



PCT10

RAW SEQUENCE LISTING

DATE: 03/11/2002

PATENT APPLICATION: US/10/069,385

TIME: 10:39:26

Input Set : A:\X-13268.App.txt

Output Set: N:\CRF3\03112002\J069385.raw

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Does A

Correc

4 <110> APPLICANT: Witcher, Derrick
 5 Tian, Yu
 6 Atkinson, Paul
 8 <120> TITLE OF INVENTION: FLINT Analog Compounds and Formulations Thereof
 10 <130> FILE REFERENCE: X-13268
 12 <140> CURRENT APPLICATION NUMBER: US/10/069,385
 13 <141> CURRENT FILING DATE: 2002-02-19
 15 <160> NUMBER OF SEQ ID NOS: 3
 17 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

77 <210> SEQ ID NO: 2
 78 <211> LENGTH: 300
 79 <212> TYPE: PRT
 80 <213> ORGANISM: Homo sapiens
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 84 1 5 10 15
 86 Ala Leu Pro Ala Leu Leu Pro Val Pro Ala Val Arg Gly Val Ala Glu
 87 20 25 30
 89 Thr Pro Thr Tyr Pro Trp Arg Asp Ala Glu Thr Gly Glu Arg Leu Val
 90 35 40 45
 92 Cys Ala Gln Cys Pro Pro Gly Thr Phe Val Gln Arg Pro Cys Arg Arg
 93 50 55 60
 95 Asp Ser Pro Thr Thr Cys Gly Pro Cys Pro Pro Arg His Tyr Thr Gln
 96 65 70 75 80
 98 Phe Trp Asn Tyr Leu Glu Arg Cys Arg Tyr Cys Asn Val Leu Cys Gly
 99 85 90 95
 101 Glu Arg Glu Glu Glu Ala Arg Ala Cys His Ala Thr His Asn Arg Ala
 102 100 105 110
 104 Cys Arg Cys Arg Thr Gly Phe Phe Ala His Ala Gly Phe Cys Leu Glu
 105 115 120 125
 107 His Ala Ser Cys Pro Pro Gly Ala Gly Val Ile Ala Pro Gly Thr Pro
 108 130 135 140
 110 Ser Gln Asn Thr Gln Cys Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala
 111 145 150 155 160
 113 Ser Ser Ser Ser Ser Glu Gln Cys Gln Pro His Arg Asn Cys Thr Ala
 114 165 170 175
 116 Leu Gly Leu Ala Leu Asn Val Pro Gly Ser Ser Ser His Asp Thr Leu
 117 180 185 190
 119 Cys Thr Ser Cys Thr Gly Phe Pro Leu Ser Thr Arg Val Pro Gly Ala

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120 195 200 205
 122 Glu Glu Cys Glu Arg Ala Val Ile Asp Phe Val Ala Phe Gln Asp Ile
 123 210 215 220
 125 Ser Ile Lys Arg Leu Gln Arg Leu Leu Gln Ala Leu Glu Ala Pro Glu
 126 225 230 235 240
 128 Gly Trp Gly Pro Thr Pro Arg Ala Gly Arg Ala Ala Leu Gln Leu Lys
 129 245 250 255
 131 Leu Arg Arg Arg Leu Thr Glu Leu Leu Gly Ala Gln Asp Gly Ala Leu
 132 260 265 270
 134 Leu Val Arg Leu Leu Gln Ala Leu Arg Val Ala Arg Met Pro Gly Leu
 135 275 280 285
 137 Glu Arg Ser Val Arg Glu Arg Phe Leu Pro Val His
 138 290 295 300
 141 <210> SEQ ID NO: 3
 142 <211> LENGTH: 936
 143 <212> TYPE: DNA
 144 <213> ORGANISM: Homo sapiens
 146 <220> FEATURE:
 147 <221> NAME/KEY: CDS
 148 <222> LOCATION: (25)..(924)
 150 <400> SEQUENCE: 3
 151 gctctccctg ctccagcaag gacc atg agg gcg ctg gag ggg cca ggc ctg 51
 152 Met Arg Ala Leu Glu Gly Pro Gly Leu
 153 1 5
 155 tgg ctg ctg tgc ctg gtg ttg gcg ctg cct gcc ctg ctg ccg gtg ccg 99
 156 Ser Leu Leu Cys Leu Val Leu Ala Leu Pro Ala Leu Leu Pro Val Pro
 157 10 15 20 25
 159 gct gta cgc gga gtg gca qaa aca ccc acc tac ccc tgg cgg gac gca 147
 160 Ala Val Arg Gly Val Ala Glu Thr Pro Thr Tyr Pro Trp Arg Asp Ala
 161 30 35 40
 163 gag aca ggg gag cgg ctg gtg tgc gcc cag tgc ccc cca ggc acc ttt 195
 164 Glu Thr Gly Glu Arg Leu Val Cys Ala Gln Cys Pro Pro Gly Thr Phe
 165 45 50 55
 167 gtg cag cgg ccg tgc cgc cga gac agc ccc acg acg tgt ggc ccg tgt 243
 168 Val Gln Arg Pro Cys Arg Arg Asp Ser Pro Thr Thr Cys Gly Pro Cys
 169 60 65 70
 171 cca ccg cgc cac tac acg cag ttc tgg aac tac ctg gag cgc tgc cgc 291
 172 Pro Pro Arg His Tyr Thr Gln Phe Trp Asn Tyr Leu Glu Arg Cys Arg
 173 75 80 85
 175 tac tgc aac qtc ctc tgc ggg gag cgt gag gag gag gca cgg gct tgc 339
 176 Tyr Cys Asn Val Leu Cys Gly Glu Arg Glu Glu Ala Arg Ala Cys
 177 90 95 100 105
 179 cac gcc acc cac aac cgt gcc tgc cgc tgc acc ggc ttc ttc gcg 387
 180 His Ala Thr His Asn Arg Ala Cys Arg Cys Arg Thr Gly Phe Phe Ala
 181 110 115 120
 183 cac gct qgt ttc tgc ttg gag cac gca tgc tgt cca cct ggt gcc ggc 435
 184 His Ala Gly Phe Cys Leu Glu His Ala Ser Cys Pro Pro Gly Ala Gly
 185 125 130 135
 187 gtg att gcc ccg ggc acc ccc agc cag aac acg cag tgc cag ccg tgc 483

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188 Val Ile Ala Pro Gly Thr Pro Ser Gln Asn Thr Gln Cys Gln Pro Cys
189          140          145          150
191 ccc cca ggc acc ttc tca gcc agc agc tcc agc tca gag cag tgc cag 531
192 Pro Pro Gly Thr Phe Ser Ala Ser Ser Ser Ser Ser Glu Gln Cys Gln
193      155          160          165
195 ccc cac cgc aac tgc acg gcc ctg ggc ctg gcc ctc att gtg cca ggc 579
196 Pro His Arg Asn Cys Thr Ala Leu Gly Leu Ala Leu Ile Val Pro Gly
197 170          175          180          185
199 tct tcc tcc cat gac acc ctg tgc acc agc tgc act ggc ttc ccc ctc 627
200 Ser Ser Ser His Asp Thr Leu Cys Thr Ser Cys Thr Gly Phe Pro Leu
201          190          195          200
203 agc acc agg gta cca gga gct gag gag tgt gag cgt gcc gtc atc gac 675
204 Ser Thr Arg Val Pro Gly Ala Glu Glu Cys Glu Arg Ala Val Ile Asp
205          205          210          215
207 ttt gtg gct ttc cag gac atc tcc atc aag agg ctg cag cgg ctg ctg 723
208 Phe Val Ala Phe Gln Asp Ile Ser Ile Lys Arg Leu Gln Arg Leu Leu
209          220          225          230
211 cag gcc ctc gag gcc ccg gag ggc tgg gct ccg aca cca agg gcg ggc 771
212 Gln Ala Leu Glu Ala Pro Glu Gly Trp Ala Pro Thr Pro Arg Ala Gly
213          235          240          245
215 cgc gcg gcc ttg cag ctg aag ctg cgt cgg cgg ctc acg gag ctc ctg 819
216 Arg Ala Ala Leu Gln Leu Lys Leu Arg Arg Arg Leu Thr Glu Leu Leu
217 250          255          260          265
219 ggg gcg cag gac ggg gcg ctg ctg gtg cgg ctg ctg cag gcg ctg cgc 867
220 Gly Ala Gln Asp Gly Ala Leu Leu Val Arg Leu Leu Gln Ala Leu Arg
221          270          275          280
223 gtg gcc agg atg ccc ggg ctg gag cgg agc gtc cgt gag cgc ttc ctc 915
224 Val Ala Arg Met Pro Gly Leu Glu Arg Ser Val Arg Glu Arg Phe Leu
225          285          290          295
227 cct gtg cac tgatcctggc cc 936
228 Pro Val His
229          300

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E--> 237 X-13268

E--> 245 1

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:82 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:2 differs:3
L:237 M:254 E: No. of Bases conflict, LENGTH:Input:-13268 Counted:938 SEQ:3
L:237 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
M:254 Repeated in SeqNo=3
L:245 M:252 E: No. of Seq. differs, <211>LENGTH:Input:936 Found:938 SEQ:3